



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Boon, Thierry; van der Bruggen, Pierre; Van den Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

(ii) TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS, TUMOR REJECTION ANTIGENS AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/819,669
(B) FILING DATE: March 17, 1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/142,368
(B) FILING DATE: May 2, 1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: December 12, 1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/764,364
(B) FILING DATE: September 23, 1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/728,838
(B) FILING DATE: July 8, 1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/705,702
(B) FILING DATE: May 23, 1991

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 5253.5 DIV. - JEL/NDH

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 688-9200
(B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	GAAGATCCTG	60
ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	CAGCCAATGA	GCTTACTGTT	120
CTCGTGGGGG	GTTCGTGAGC	CTTGGGTAGG	AAGTTTGCA	AGTTCCGCT	ACAGCTCTAG	180
CTTGTGAATT	TGTACCCCTT	CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	240
CCCCCTCCCA	CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCCCTT	GCTCTCCAG	CATGCATTGT	360
GTCAACGCCA	TTGCACTGAG	CTGGTGAAG	AAGTAAGCCG	CTAGCTTGC	ACTCTACTCT	420
TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	ACCCTTTGTG	CC		462

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT	8	
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly		
5	10	15

GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
 20 25 30

GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
 35 40 45

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AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
      50           55           60

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TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
   65           70           .           75           80

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TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAC TAC TAC	288
Ser Val Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr	
85 90 95	
GAC GAC GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	336
Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp	
100 105 110	
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAA TCA GAA GAT GAG	384
Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu	
115 120 125	
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met	
130 135 140	
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys	
145 150 155 160	
AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe	
165 170 175	
CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT	576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys	
180 185 190	
GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG	624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu	
195 200 205	
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	672
Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro	
210 215 220 225	
TAG	675

(2) INFORMATION FOR SEQUENCE ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTT	60
TTCCCCCTTCA TTAATTTCT AGTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT	120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC	180

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGG GTTTGTGAGC CTTGGGTAGG	150
AAGTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCCTCCCA	250
CCTCGTCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCCTTGCG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT	966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
TTGTTTTTT TTCCCTTCATTAATTCT AGTTTTAGT AATCCAGAAA	1237
ATTTGATTTT GTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
GTAAAATA AAAGTTGAC TTGCATAC	1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCACTCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGG GTTGTGAGC CTTGGTAGG	150
AAGTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
CCTCGTCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCCTTGCG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTA	966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
CCCCACTCCT TGCTCCGCTC TCTTTCTTT TCCCACCTTG CCTCTGGAGC	1116
TTCAGTCCAT CCTGCTCTGC TCCCTTCCC CTTTGCTCTC CTTGCTCCCC	1166
TCCCCCTCGG CTCAACTTTT CGTGCCTCT GCTCTCTGAT CCCCACCCCTC	1216
TTCAGGCTTC CCCATTGCT CCTCTCCCGA AACCCCTCCCC TTCTGTTCC	1266
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
TCACCAAGCTT TGCTCTCCCT GCTCCCTCC CCCTTTGCA CCTTTTCTTT	1366
TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCCTTCAC CGCTTTCCCT	1416
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTG CATTTCGGG	1466
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTCGATT TTCGGGTGCT	1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566
TGTTTTTTC GAGACAGGGT TTCTCTTGT ATCCCTGGCT GTCCTGGCAC	1616
TCACTCTGTA GACCAGGCTG GCCTCAAAC T CAGAAATCTG CCTGCCTCTG	1666
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG	1716
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT	1766
AACTCCCCCTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCCTCCCTGT	1816
TTCCCTTCG GCACCCCTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC	1866
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGTTTCT	1916
CCCCCGTTCC CCTTTTTGT GCCTTCTCTC CTGGCTCCCC TCCACCTCC	1966

AGCTCACCTT	TTTGGTTGTT	TGGGTTGTTG	GTTGGTTGGT	TTGCTTTTT	2016
TTTTTTTTT	GCACCTGTT	TTCCAAGATC	CCCTCTCCCC	CCCGGCTTCC	2066
CCTCTGTGTG	CCTTCTCTGT	TCCCTCCCCC	TCGCTGGCTC	CCCCTCCCTT	2116
TCTGCCTTTC	CTGTCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTT	2166
CTTTTCTAGA	CTCCCCCTC	CAGGCTTGCT	GTTGCTTCT	GTGCACTTT	2216
CCTGACCTG	CTCCCCCTCC	CCTCCCAGCT	CCCCCCTCTT	TTCCCACCTC	2266
CCTTCTCCA	GCCTGTCACC	CCTCCTCTC	TCCTCTCTGT	TTCTCCCACT	2316
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
GACTTCCTCT	CCAGCCGCC	AGTCCCTGTC	AGTCCTGGAG	TCTTCTCTGC	2416
CTCTCTGTCC	ATCACTTCCC	CCTAGTTCA	CTTCCCTTT	ACTCTCCCT	2466
ATGTGTCTCT	CTTCCTATCT	ATCCCTTCT	TTCTGTCCCC	TCTCCTCTGT	2516
CCATCACCTC	TCTCCTCCCT	TCCCTTCTCT	CTCTCTTCCA	TTTTCTTCCA	2566
CCTGCTTCTT	TACCCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616
TCCATGTCCC	CTCTCAATT	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
TTCCCTTTGC	TTCTCCCTCC	TCCCTTCCCC	TTCCCTATG	CCCTCTACTC	2766
TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTCCCTTT	CCACCCGCC	2816
CTTTGTCCCC	AGACCCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
ATCAACAAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCCAA	ATCAGCAGGA	2916
AAGGCTGGAT	GAAAATAAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
AAAGTGGCTCC	TATAACCCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAATG	3066
CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
GAATCTGAAA	ACTAGGGGCC	AGTGGTTGT	TTTGGGGACA	AATTAGCACG	3166
TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACATATGAA	GTTCTTTTA	3266
GGCTAAAGAT	ACTTGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
TTGCTAAAAT	ATTCTTCTC	ACATATTCA	ATTCTCCAG		3355
GT	GTT	CCT	GGC	CAT	3396
AGG	ATG	ATT	TAT	TTC	3438
ATA	CCA	GTG	AAC	CCT	3480
AAT	GCT	GAT	GAA	GAG	3522
GAG	GAG	GAG	GAG	GAA	3564
TTC	TCA	CCT	TAG		3576
GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCTAACA	TATGCCGT	3626
GCTAAGAGCA	TCTTTTAAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
TCTTTTACA	TTAATAAGTA	TTAAATTAA	CCAGTATACA	GTCTTAAGAA	3726
CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCGT	TCTTTAGATT	3776
GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
GACCAAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
TTCTTATAGT	ACCTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
TTCAAGAAAG	ATCACACGCC	ATGGTTCAC	TGCAAATTAT	TATTTTGTG	3976
TTCTGATTTT	TTTCATTCT	AGACCTGTGG	TTTAAAGAG	ATGAAAATCT	4026
CTTAAAATTT	CCTTCATCTT	TAATTTCT	TAACTTAGT	TTTTTCACT	4076
TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTA	GATTTCTAA	4126
AATGTTTTT	AAAAAAATG	CAAATCTCAT	TTTTAAGAGA	TGAAAGCAGA	4176
GTAACGGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTG	4276
CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
ATAAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
AGTCAGGAGT	GTATTCTAAT	AAGTGTGCT	TATCTCTTAT	TTTCTTCTAC	4476
AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTT	4526
TTTTTCCCTT	TTCATTAATT	TTCTAGTTT	TAGTAATCCA	AAAAATTGA	4576

TTTTGTTCTA AAGTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT	4626
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA	4676
AATAAAAGTT TGACTTGCAT AC	4698

(2) INFORMATION FOR SEQUENCE ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu

5

(2) INFORMATION FOR SEQUENCE ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG	50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC	100
TCCTGGTAGC ACTGAGAAC CAGGGCTGTG CTTGCGGTCT GCACCCCTGAG	150
GGCCCGTGGG TTCCTCTTCC TGGAGCTCCA GGAACCAAGGC AGTGAGGCCT	200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT	250
GCCAGCAGTG AATGTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT	350
CCTGTAGAAC CGACCTCTGC TGGCCGGCTG TACCCCTGAGT ACCCTCTCAC	400
TTCCTCCTTC AGGTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC	450
CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTG	500
TTAGAGTCTC CAAGGTTCAAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT	550
CTCTCCCCAG GCCTGTGGGT CTTCATGCC CAGCTCCTGC CCACACTCCT	600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC	650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCC AACAAAGAGGC CCTGGGCCTG	700
GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGCAC	750
CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCTCTC	800
AGGGAGCCTC CGCCTTCCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA	850
CCCAGTGAGG GTTCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTG	900
TATCCTGGAG TCCTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT	950
TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG	1000
GCAGAAATGC TGGAGAGTGT CATAAAAAT TACAAGCACT GTTTCTGA	1050

GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCCACC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAAGA	1350
TTTGGTGCAG	GAAAAGTACC	TGGAGTACCG	GCAGGTGCG	GACAGTGATC	1400
CCGCACGCTA	TGAGTTCCCTG	TGGGGTCCAA	GGGCCCTCGC	TGAAACCAGC	1450
TATGTGAAAG	TCCTTGAGTA	TGTGATCAAG	GTCAGTCAA	GAGTCGCTT	1500
TTTCTTCCA	TCCCTGCGTG	AAGCAGCTTT	GAGAGAGGAG	GAAGAGGGAG	1550
TCTGAGCATG	AGTTGCAGCC	AAGGCCAGTG	GGAGGGGGAC	TGGGCCAGTG	1600
CACCTTCCAG	GGCCCGTCC	AGCAGCTTCC	CCTGCCTCGT	GTGACATGAG	1650
GCCCATTCTT	CACTCTGAAG	AGAGCGGTCA	GTGTTCTCAG	TAGTAGGTTT	1700
CTGTTCTATT	GGGTGACTTG	GAGATTATC	TTTGTCTCT	TTTCCAATTG	1750
TTCAAATGTT	TTTTTTAAG	GGATGGTTGA	ATGAACTTCA	GCATCCAAGT	1800
TTATGAATGA	CAGCAGTCAC	ACAGTTCTGT	GTATATAGTT	TAAGGGTAAG	1850
AGTCTTGTGT	TTTATTCAAGA	TTGGGAAATC	CATTCTATT	TGTGAATTGG	1900
GATAATAACA	GCAGTGGAAAT	AAGTACTTAG	AAATGTGAAA	AATGAGCAGT	1950
AAAATAGATG	AGATAAAGAA	CTAAAGAAAT	TAAGAGATAG	TCAATTCTTG	2000
CCTTATAACCT	CAGTCTATT	TGTAAAATTT	TTAAAGATAT	ATGCATACCT	2050
GGATTTCCCTT	GGCTCTTTG	AGAATGTAAG	AGAAATTAAA	TCTGAATAAA	2100
GAATTCTTCC	TGTCACTGG	CTCTTTCTT	CTCCATGCAC	TGAGCATCTG	2150
CTTTTTGAA	GGCCCTGGGT	TAGTAGTGG	GATGCTAAGG	TAAGCCAGAC	2200
TCATACCCAC	CCATAGGGTC	GTAGAGTCTA	GGAGCTGCAG	TCACGTAATC	2250
GAGGTGGCAA	GATGTCCTCT	AAAGATGTAG	GGAAAAGTGA	GAGAGGGGTG	2300
AGGGTGTGGG	GCTCCGGGTG	AGAGTGGTGG	AGTGTCAATG	CCCTGAGCTG	2350
GGGCATTTTG	GGCTTTGGGA	AACTGCAGTT	CCTCTGGGG	GAGCTGATTG	2400
TAATGATCTT	GGGTGGATCC				2420

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCGGGGCAC	CACTGGCATC	CCTCCCCCTA	CCACCCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGAGGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCCAG	CCCCCTTGCT	GCTTAAACCA	400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGTTAGG	450

AGAGGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
ATGCTCACTC	CCGTGACCCA	ACCCCCTTT	CATTGTCATT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCAGCC	650
ATTCCACCCCT	CACCCCCACC	CCCACCCCCA	CGCCCACTCC	CACCCCCACC	700
CAGGCAGGAT	CCGGTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
AGGGACGGCG	TAGAGTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCCGCC	ACTCCAAATA	900
GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCACC	950
CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCCAC	CCCATTGCA	TTCCCATTCC	CCACCCAACC	1200
CCCATCTCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
TCACCCCTCAC	TGCCCCAAC	CCCACCCCTA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTCT	GGCAGAATCC	GGTTTGCC	TGCTCTAAC	1400
CAAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	CGGGCTTGAG	1500
ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGTAGATGG	CCCCAAATG	1600
ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATH	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCCTGGGAG	GGAACCTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCCATACCT	ACCCCTTACC	CCCAACCTCA	1900
TCTTGTCA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAGGG	2000
GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC	AGAGGACCCA	GCACCCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACCGCG	AGGAAGAGGA	2200
GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
CTGCCCCCTT	TTAGTAGCTC	TAGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
GTTGAGGAA	GCACAGGCC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTCAGC	CCTGGACACC	2700
TCACCCAGGA	TGTGGCTTCT	TTTCACCTCC	TGTTTCCAGA	TCTGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTGGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCAG	GACCAGAAC	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCCTGCTGT	CACCCAGAG	AGCATGGCT	2950
GGGCCGTCTG	CCGAGGTCTT	TCCGTTATCC	TGGGATCATT	GATGTAGGG	3000
ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCA	TAGAGGGAGC	3050
GTCCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
CAGGACACAT	TAATCCAAT	GAATTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150

AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCCTCCT	GTCCTTCAT	3200
TCCTTATCAT	GGATGTGAAC	TCTTGATTTG	GATTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
CACCCCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
GCCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCCT	3650
CTCACTTCCT	CCTTCAGGTT	TTCAGGGAC	AGGCCAACCC	AGAGGACAGG	3700
ATTCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3750
CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCAGCT	CCTGCCACA	3850
CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA					3922
GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG					3964
CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC					4006
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG					4048
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC					4090
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA					4132
GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC					4174
CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT					4216
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA					4258
GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT					4300
CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG CAG CTG GTC					4342
TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC					4384
TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG					4426
CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA					4468
ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT					4510
GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT					4552
GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG					4594
CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC CGG					4636 --
CAG GTG CCG GAC AGT GAT CCC GCA CGC TAT GAG TTC CTG TGG					4678
GGT CCA AGG GCC CTC GCT GAA ACC AGC TAT GTG AAA GTC CTT					4720
GAG TAT GTG ATC AAG GTC AGT GCA AGA GTT CGC TTT TTC TTC					4762
CCA TCC CTG CGT GAA GCA GCT TTG AGA GAG GAG GAA GAG GGA					4804
GTC TGA					4810
GCATGAGTTG	CAGCCAAGGC	CAGTGGGAGG	GGGACTGGGC	CAGTGCACCT	4860
TCCAGGGCCG	CGTCCAGCAG	CTTCCCTGC	CTCGTGTGAC	ATGAGGCCA	4910
TTCTTCACTC	TGAAGAGAGC	GGTCAGTGT	CTCAGTAGTA	GGTTTCTGTT	4960
CTATTGGGTG	ACTTGGAGAT	TTATCTTGT	TCTCTTTGG	AATTGTTCAA	5010
ATGTTTTTT	TTAAGGGATG	GTTGAATGAA	CTTCAGCATC	CAAGTTTATG	5060
AATGACAGCA	GTCACACAGT	TCTGTGTATA	TAGTTTAAGG	GTAAGAGTCT	5110
TGTGTTTTAT	TCAGATTGGG	AAATCCATT	TATTTGTGA	ATTGGGATAA	5160
TAACAGCAGT	GGAATAAGTA	CTTAGAAATG	TGAAAAATGA	GCAGTAAAAT	5210
AGATGAGATA	AAGAACTAAA	GAAATTAAGA	GATAGTCAT	TCTTGCCTTA	5260
TACCTCAGTC	TATTCTGTAA	AATTTTAAA	GATATATGCA	TACCTGGATT	5310
TCCTTGGCTT	CTTGAGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAAGAATT	5360
CTTCCTGTC	ACTGGCTTT	TTCTTCTCCA	TGCACTGAGC	ATCTGCTTT	5410
TGGAAGGCC	TGGGTTAGTA	GTGGAGATGC	TAAGGTAAGC	CAGACTCATA	5460
CCCACCCATA	GGGTCGTAGA	GTCTAGGAGC	TGCACTCAGC	TAATCGAGGT	5510
GGCAAGATGT	CCTCTAAAGA	TGTAGGGAAA	AGTGAGAGAG	GGGTGAGGGT	5560
GTGGGGCTCC	GGGTGAGAGT	GGTGGAGTGT	CAATGCCCTG	AGCTGGGGCA	5610

TTTTGGGCTT TGGGAAACTG CAGTTCCCTTC TGGGGGAGCT GATTGTAATG	5660
ATCTTGGGTG GATCC	5675

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA TCCCCATCCG GGCAGAACCC	50
CCCAGGGAAAG TCACGGGCC	100
GGTCAGAGGA CAGCGAGATT	150
GAGGGAAAGCA GGCGCAGGCT	200
AGGACTGAGG CGGGCCTCAC	250
GCTGCCTCTG CTGCCGGGCC	300
GCTCAGTCGC CACCACCTCA	350
GGAACCTCTGG CGTAAGAGCT	400
TGCTCAGGGC CCAGACTCG	450
GAATGAGGGC AACCCACCCC	500
ACCAACCCCCA CCCCCATCCC	550
TCCCCATCTCC TCCCCCACCA	600
CAATCAACCC ACGGAAGCTC	650
ACGTTCACAT GTACGGCTAA	700
GGCCTTTGGG ATGCAGAGGA	750
TCCTTAGGGG ACCCAGCATG	800
TCAAACCTGAG CCACCTTTTC	850
CCCACCTTCAG GGGTTGGGG	900
AAGAGGGAGG ACTGAGGGGA	950
GCTGGGGGAT CCTGGGCACA	1000
CTTCAGGGTG ACAGAGAGTT	1050
GGTCAGCAGA GGGAGGAATC	1100
CTTCATGAGG ACTCCCCATA	1150
AGTCTGGAAG TAAATTGTT	1200
CCCTAAGTGA CAATTCATT	1250
CAGGGAGATA AGGTGTTGGT	1300
GGTTCCCCCT TGAGAAAGGG	1350
CCACAGGAGG CCATCATAAC	1400
GGACAACGCA CGTGGGGTAA	1450
CAGATCTCAG GGAGTTGATG	1500
ACAGGGGCC CTCGGTCGA	1550
ATCCAGGTGG AGAGCCTGAG	1600
GCAGCAAGGG GGCCCCATAG	1650
AGACCCCTGGG CAGGGCTGTC	1700
TGATGTCAGG GAAGGGGAGG	1750
CCTTGGTCTG AAGGGGCTGG	
AGTCAGGTCA	

GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTGAC	ATCTCTCGTT	1850
GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATT	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTC	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCGCACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT GAG CAG AGG AGT	CAG CAC TGC AAG CCT	GAA GAA	ATG CCT CTT GAG CAG AGG AGT	CAG CAC TGC AAG CCT	2639
GGC CTT GAG GCC CGA GGA GAG	GCC CTG GGC CTG GTG	GGT GCG	GGC CTT GAG GCC CGA GGA GAG	GCC CTG GGC CTG GTG	2681
CAG GCT CCT GCT ACT GAG GAG	CAG CAG ACC GCT	TCT TCC TCT	CAG GCT CCT GCT ACT GAG GAG	CAG CAG ACC GCT	2723
TCT ACT CTA GTG GAA GTT ACC	CTG GGG GAG GTG	CCT GCT GCC	TCT ACT CTA GTG GAA GTT ACC	CTG GGG GAG GTG	2765
GAC TCA CCG AGT CCT CCC CAC	AGT CCT CAG GGA	GCC TCC AGC	GAC TCA CCG AGT CCT CCC CAC	AGT CCT CAG GGA	2807
TTC TCG ACT ACC ATC AAC TAC	ACT CCT TTT TGG	AGA CAA TCC GAT	TTC TCG ACT ACC ATC AAC TAC	ACT CCT TTT TGG	2849
GAG GGC TCC AGC AAC CAA GAA	GAG GAG GGG CCA	AGA ATG TTT	GAG GGC TCC AGC AAC CAA GAA	GAG GGG CCA	2891
CCC GAC CTG GAG TCC GAG	TTC CAA GCA GCA	ATC AGT AGG AAG	CCC GAC CTG GAG TCC GAG	TTC CAA GCA GCA	2933
ATG GTT GAG TTG GTT CAT TTT	CTG CTC CTC AAG	TAT CGA GCC	ATG GTT GAG TTG GTT CAT TTT	CTG CTC CTC AAG	2975
AGG GAG CCG GTC ACA AAG GCA	GAA ATG CTG GAG	AGT GTC CTC	AGG GAG CCG GTC ACA AAG GCA	GAA ATG CTG GAG	3017
AGA AAT TGC CAG GAC TTC TTT	CCC GTG ATC TTC	AGC AAA GCC	AGA AAT TGC CAG GAC TTC TTT	CCC GTG ATC TTC	3059
TCC GAG TAC TTG CAG CTG GTC	TTT GGC ATC GAG	GTG GTG GAA	TCC GAG TAC TTG CAG CTG GTC	TTT GGC ATC GAG	3101
GTG GTC CCC ATC AGC CAC TTG	TAC ATC CTT GTC	ACC TGC CTG	GTG GTC CCC ATC AGC CAC TTG	TAC ATC CTT GTC	3143
GGC CTC TCC TAC GAT GGC CTG	CTG GGC GAC AAT	CAG GTC ATG	GGC CTC TCC TAC GAT GGC CTG	CTG GGC GAC AAT	3185
CCC AAG ACA GGC CTC CTG ATA	ATC GTC CTG GCC	ATA ATC GCA	CCC AAG ACA GGC CTC CTG ATA	ATC GTC CTG GCC	3227
ATA GAG GGC GAC TGT GCC CCT	GAG AAA ATC TGG GAG	GAG	ATA GAG GGC GAC TGT GCC CCT	GAG AAA ATC TGG GAG	3269
CTG AGT ATG TTG GAG GTG	TTT GAG GGG AGG GAG	GAC AGT GTC	CTG AGT ATG TTG GAG GTG	TTT GAG GGG AGG GAG	3311
TTC GCA CAT CCC AGG AAG CTG	CTC ATG CAA GAT	CTG GTG CAG	TTC GCA CAT CCC AGG AAG CTG	CTC ATG CAA GAT	3353
GAA AAC TAC CTG GAG TAC CGG	CAG GTG CCC GGC	AGT GAT CCT	GAA AAC TAC CTG GAG TAC CGG	CAG GTG CCC GGC	3395
GCA TGC TAC GAG TTC CTG	TGG GGT CCA AGG	GCC CTC ATT GAA	GCA TGC TAC GAG TTC CTG	TGG GGT CCA AGG	3437
ACC AGC TAT GTG AAA GTC CTG	CAC CAT ACA CTA	AAG ATC GGT	ACC AGC TAT GTG AAA GTC CTG	CAC CAT ACA CTA	3479
GGA GAA CCT CAC ATT TCC TAC	CCA CCC CTG CAT	GAA CGG GCT	GGA GAA CCT CAC ATT TCC TAC	CCA CCC CTG CAT	3521
TTG AGA GAG GGA GAA GAG	TGA		TTG AGA GAG GGA GAA GAG	TGA	3542
GTCTCAGCAC ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	GTCTCAGCAC ATGTTGCAGC	CAGGGCCAGT	3592
GCACCTTCCA GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	GCACCTTCCA GGGCCCCATC	CATTAGCTTC	3642
GGCCCCATTCC TGCCCTTTG	AAGAGAGCAG	TCAGCATTCT	GGCCCCATTCC TGCCCTTTG	AAGAGAGCAG	3692
TTTCTGTTCT GTTGGATGAC	TTTGAGATT	ATCTTTCTTT	TTTCTGTTCT GTTGGATGAC	TTTGAGATT	3742
TTGTTCAAAT GTTCCTTTA	ACAAATGGTT	GGATGAACTT	TTGTTCAAAT GTTCCTTTA	ACAAATGGTT	3792
GTTTATGAAT GACAGTAGTC	ACACATAGTG	CTGTTTATAT	GTTTATGAAT GACAGTAGTC	ACACATAGTG	3842
TAAGAGTCCT GTTTTTATT	CAGATTGGGA	AATCCATTCC	TAAGAGTCCT GTTTTTATT	CAGATTGGGA	3892
TTGTCACATA ATAACAGCAG	TGGAATATGT	ATTTGCCTAT	TTGTCACATA ATAACAGCAG	TGGAATATGT	3942
AATTAGCAGT AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AATTAGCAGT AAAATACATG	ATACAAGGAA	3992
TGCCTTATAC CTCAGTCTAT	TATGTAAAAT	TAAAATATG	TGCCTTATAC CTCAGTCTAT	TATGTAAAAT	4042
TGCTTCTTTG AGAATGCAA	AGAAATTAAA	TCTGAATAAA	TGCTTCTTTG AGAATGCAA	AGAAATTAAA	4092
TCACTGGCTC ATTTCTTAC	CATTCACTCA	GCATCTGCTC	TCACTGGCTC ATTTCTTAC	CATTCACTCA	4142
CCTGGTAGTA GTGGG			CCTGGTAGTA GTGGG		4157

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCCCCAT GGATCCAGGA AGAATCCAGT TCCACCCCTG CTGTGAACCC	50
AGGGAAAGTCA CGGGGCCGGA TGTGACGCCA CTGACTTGCG CGTTGGAGGT	100
CAGAGAACAG CGAGATTCTC GCCCTGAGCA ACGGCCTGAC GTCGGCGGAG	150
GGAAGCAGGC GCAGGCTCCG TGAGGAGGCA AGGTAAGATG CCGAGGGAGG	200
ACTGAGGCGG GCCTCACCCCC AGACAGAGGG CCCCCAATAA TCCAGCGCTG	250
CCTCTGCTGC CAGGCCTGGA CCACCCCTGCA GGGGAAGACT TCTCAGGCTC	300
AGTCGCCACC ACCTCACCCCC GCCACCCCCC GCGCTTTAA CCGCAGGGAA	350
CTCTGGTGTA AGAGCTTGT GTGACCAAGGG CAGGGCTGGT TAGAAGTGCT	400
CAGGGCCAG ACTCAGCCAG GAATCAAGGT CAGGACCCCCA AGAGGGGACT	450
GAGGGTAACC CCCCCGCACC CCCACCACCA TTCCCATCCC CCAACACCAA	500
CCCCACCCCCC ATCCCCAAC ACCAAACCCA CCACCATCGC TCAAACATCA	550
ACGGCACCCCC CAAACCCCCGA TTCCCATCCC CACCCATCCT GGCAGAATCG	600
GAGCTTGCC CCTGCAATCA ACCCACGGAA GCTCCGGGAA TGGCGGCCAA	650
GCACGCGGAT CC	662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG	50
GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
AGATCTGCCA GTGGGTCTCC ATTGCCAGC TCCTGCCAC ACTCCCGCCT	150
GTTGCCCTGA CCAGAGTCAT C	171
ATG CCT CTT GAG CAG AGT CAG CAC TGC AAG CCT GAA GAA	213
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	255
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	297
TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	339

GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	381
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	465
CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG	507
GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
TTG AGA GAG GGG GAA GAG TGA	1116
GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
GCACCTTCGG GGGCGCGATC CCTTAGTTTC CACTGCCCTCC TGTGACGTGA	1216
GGCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
TTGTTCAAAT GTTCCTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
TTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTATAT AGTTTAGGAG	1416
TAAGAGTCTT GttTTTTACT CAAATTggGA AATCCATTCC ATTTTGAA	1466
TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTGCTTAA AATTGTGAGC	1516
GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
ATTCTTGCTT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
ACCAGGATTG CCTTGACTTC TTTG	1640

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-31 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCCAAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT	50
CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG	100
GCCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG	150
AGGACTTGGT CTGAGGGAGT GTCCCTCAGGT CACAGAGTAG AGGGGGCTCA	200
GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC	250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT	300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC	350

CTCTCACTTC	CTCCTTCAGG	TTCTGAGGGG	ACAGGCTGAC	CTGGAGGACC	400
AGAGGCCCCC	GGAGGAGCAC	TGAAGGAGAA	GATCTGTAAG	TAAGCCTTG	450
TTAGAGCCTC	CAAGGTTCCA	TTCAGTACTC	AGCTGAGGTC	TCTCACATGC	500
TCCCTCTCTC	CCCAGGCCAG	TGGGTCTCCA	TTGCCAGCT	CCTGCCACAA	550
CTCCCGCCCTG	TTGCCCTGAC	CAGAGTCATC			580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA					622
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG					664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT					706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC					748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC					790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT					832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC					874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG					916
GTG GCC AAG TTG GTT CAT TTT CTG CTC					943

(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	39
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	81
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	123
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	165
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	207
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	249
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	291
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	333
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	375
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	417
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	459
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	501
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	543
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	585
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	627
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	669
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGCAGG GCTGGGCCAG	719
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	769
GCCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG	819
GTTTCTATTGTTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	869
ATTGTTGAAA TGTTCCCTTTT AATGGATGGT TGAATTAAC TCAAGCATCCA	919
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTAAATATA GTTTAGGAGT	969
AAGAGTCTTG TTTTTTATTC AGATTGGAA ATCCGTTCTA TTTTGTGAAT	1019

(2) INFORMATION FOR SEQUENCE ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: MAGE-5 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT	50
AAGCCTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA GGCTTCTCAC	100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCC AGCTCCTGCC	150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	226

(2) INFORMATION FOR SEQUENCE ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: MAGE-6 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG	42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC	84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC	126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC	168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC	210
TGT GCC CCT GAG GAG	225

(2) INFORMATION FOR SEQUENCE ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-7 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG 42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC 84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC 126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A 166

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